AMENDMENTS TO THE CLAIMS

1. (Cancelled).

2. (Previously presented) The method of claim 20 wherein the amplification is carried out using a thermostable nucleic acid polymerase.

3. (Previously presented) The method of claim 20 wherein the fluorophore on the first probe and the quencher molecule on the second probe are on complementary base pairs.

4. (Previously presented) The method of claim 20 wherein the fluorophore and quencher molecules are within about 1 to 3 hybridized base pairs of each other.

5. (Previously presented) The method of claim 20 wherein the fluorophore and quencher molecules are within 3 or more hybridized base pairs of each other.

6. (Previously presented) The method of claim 20 wherein the fluorophore is on the 5' terminal nucleotide of the first probe and the quencher is on the 3' terminal nucleotide of the second probe.

7. (Previously presented) The method of claim 20 wherein the fluorophore is on the 3' terminal nucleotide of the first probe and the quencher is on the 5' terminal nucleotide of the second probe.

8. (Currently amended) The method of claim 20 wherein the second probe is shorter than the first probe ~~by deletion of 3 or 3' terminal nucleotides from the nucleotide sequence of the first probe~~.

9. (Currently amended) The method of claim **[[20]]** **8** wherein the second probe is **at least three nucleotides** shorter than the first probe ~~by deletion of 3 or more 3' terminal nucleotides from the nucleotide sequence of the first probe~~.

10. (Cancelled).

11. (Previously presented) The method of claim 20 wherein the first and second probes have a dissociation temperature difference of 2 degrees or more.

12-13. (Cancelled).

14. (Previously presented) The method of claim 20 wherein the first probe has the sequence of SEQ ID NO. 3.

15. (Previously presented) The method of claim 20 wherein the first probe has the sequence of SEQ ID NO. 4.

16. (Previously presented) The method of claim 20 wherein the amplification method is the polymerase chain reaction and wherein a primer for use in the polymerase chain reaction has the sequence of SEQ ID NO. 1.

17. (Previously presented) The method of claim 20 wherein the amplification method is the polymerase chain reaction and wherein a primer for use in the polymerase chain reaction has the sequence of SEQ ID NO. 2.

18. (Currently amended) The method of claim 20 wherein the target ~~**polynucleotide is a polynucleotide comprising**~~ **nucleic acid comprises** the hepatitis C virus genome or segment thereof.

19. (Currently amended) The method of claim 20 wherein the method of amplification is selected from the group consisting of **polymerase chain reaction,** ligase chain reaction, gap ligase chain reaction, transcription mediated amplification, nucleic acid sequence based amplification and strand displacement amplification.

20. (Currently amended) A method for **real-time** monitoring **of** nucleic acid amplification comprising:

amplifying a target nucleic acid and monitoring said target nucleic acid during said amplification using a first oligonucleotide probe and a second oligonucleotide probe,

said first probe;

i) ~~hybridizes~~ **is capable of hybridizing** to said target nucleic acid;

ii) comprises a fluorophore; and

iii) is not equal in length to said second probe;

said second probe;

i) ~~hybridizes~~ **is capable of hybridizing** to said first probe; and

ii) has a quencher molecule which quenches said first probe fluorophore when said first and second probes are hybridized to each other; and

detecting fluorescence of said first probe fluorophore **in real-time** to monitor amplification, wherein an increase in fluorescence correlates with amplification.

21. (Previously presented) The method of claim 20 wherein the amplification method includes the use of a primer pair that flanks the first and second probe.

22. (Previously presented) The method of claim 20 wherein the longer probe binds preferentially to the target polynucleotide and when preferentially bound to the target polynucleotide the fluorescence intensity of the fluorophore is greater than the fluorescence intensity of the fluorophore when hybridized to the second probe.

23. (New) A method for monitoring nucleic acid amplification comprising:

(i) amplifying a target nucleic acid in a cycling amplification reaction in the presence of a first probe and a second probe;

said first probe;

i) is capable of hybridizing to said target nucleic acid;

ii) comprises a fluorophore; and

iii) is not equal in length to said second probe;

said second probe;

i) is capable of hybridizing to said first probe; and

ii) has a quencher molecule which quenches said first probe fluorophore when said first and second probes are hybridized to each other; and

(ii) assessing the amount of amplified target nucleic acid produced by said amplification reaction by detecting the amount of fluorescence of said first probe fluorophore during a plurality of cycles of said amplification reaction, wherein the amount of fluorescence correlates with the amount of amplified target nucleic acid.

24. (New) The method of claim 23 wherein the fluorophore on the first probe and the quencher molecule on the second probe are on complementary base pairs.

25. (New) The method of claim 23 wherein the fluorophore and quencher molecules are within about 1 to 3 hybridized base pairs of each other.

26. (New) The method of claim 23 wherein the fluorophore is on the 5' terminal nucleotide of the first probe and the quencher is on the 3' terminal nucleotide of the second probe.

27. (New) The method of claim 23 wherein the fluorophore is on the 3' terminal nucleotide of the first probe and the quencher is on the 5' terminal nucleotide of the second probe.

28. (New) The method of claim 23 wherein the second probe is shorter than the first probe.

29. (New) The method of claim 28 wherein the second probe is at least three nucleotides shorter than the first probe.

30. (New) The method of claim 23 wherein the first and second probes have a dissociation temperature difference of 2 degrees or more.

31. (New) The method of claim 23 wherein the first probe has the sequence of SEQ ID NO. 3.

32. (New) The method of claim 23 wherein the first probe has the sequence of SEQ ID NO. 4.

33. (New) The method of claim 23 wherein the amplification reaction is the polymerase chain reaction and wherein a primer for use in the polymerase chain reaction has the sequence of SEQ ID NO. 1.

34. (New) The method of claim 23 wherein the amplification reaction is the polymerase chain reaction and wherein a primer for use in the polymerase chain reaction has the sequence of SEQ ID NO. 2.

35. (New) The method of claim 23 wherein the target nucleic acid comprises at least a segment of the hepatitis C virus genome.

36. (New) The method of claim 23 wherein the method of amplification is selected from the group consisting of polymerase chain reaction, ligase chain reaction, gap ligase chain reaction, transcription mediated amplification, nucleic acid sequence based amplification and strand displacement amplification.

37. (New) The method of claim 23 wherein the amplification reaction includes the use of a primer pair that flanks the first and second probe.

38. (New) The method of claim 23, wherein the fluorescence of said first probe fluorophore is detected during every cycle of said amplification reaction.